IN THE SPECIFICATION:

Please amend the specification as shown:

Please delete paragraph [00038] on page 100, and replace it with the following paragraph:

[00038] Figure 2 illustrates three alternative splice variants of the iPLA$_2\gamma$ gene. Gamma 1 is shown in Row 1, Gamma 2 is shown in Row 2 and Gamma 3 is shown in Row 3. Open boxes are noncoding regions, shaded regions are putative coding regions and stippled lines represent intron splicing.

Please delete paragraph [00046] on page 11, and replace it with the following paragraph:

[00046] Figure 10 shows a potential alternative exon 5 splice variant of human iPLA$_2\gamma$. Row 1 shows 'A' reported splice sequence (gc/ag), source (Tanaka et al.) BBRC 272:320, 2000. Row 2 shows 'B' potential splice variant (gt/ag), source (Gross lab) JBC 275:9937, 2000. The incidence of gc/ag splice variants like the one shown in 'A' is 0.56%. The variant 'A' has been reported in the literature, reported in GenBank, and cloned in our lab. The splice variant gt/ag occurs with a frequence of 98.71% among genes. However, variant 'B' iPLA$_2\gamma$ sequence has not been cloned. In gene splicing, introns typically begin with the dinucleotide "gt" and end with "ag". This gt/ag splice signal occurs with a frequency of 98.71% in gene splicing and can be used as a reliable tool for identifying the boundaries of exons in genes. The previously reported 3' splice signal of iPLA$_2\gamma$ exon 5 is illustrated in 'A'. This splice site utilizes an unusual gc/ag splice signal which is utilized at a frequency of only 0.56% in splicing of genes. The use of the more common gt/ag splice signal will result in splicing shown in 'B'. As illustrated, this splicing will not alter the reading frame of the encoded protein but will result in a modified portion of the iPLA$_2\gamma$ sequence which contains the sequence "ASCSV" (SEQ ID NO: 28) in place of "IIAR" (SEQ ID NO: 51) shown in 'A'. Sequence encoding the altered sequence in 'B' has not yet been cloned from a cDNA library

nor has sequence with identity to SEQ ID NO: 28 been reported in GenBank® (NIH genetic sequence database). However, because of the extensive alternative splicing that the iPLA$_2\gamma$ gene undergoes (at least 10 splice variants), it is at least plausible that the more common gt/ag splicing may be utilized at the 3' end of exon 5 resulting in a polypeptide containing SEQ ID NO: 28. Because of the proximity of the amino acids affected by this alternative splicing to the lipase consensus site (within 126 amino acids), the generation of a polypeptide with SEQ ID NO: 28 could potentially result in modulation of iPLA$_2\gamma$ activity or functional properties.

Please delete paragraph [00049] on page 12, and replace it with the following paragraph:

[00049] Figure 13 is a schematic illustration of the genomic organization of the human iPLA$_2\gamma$ gene. The *5' of exon2 end has also been reported as nucleotides 133114 and 133464 in GenBank.

Please delete paragraph [00058] on pages12-13, and replace it with the following paragraph:

[00058] Figure 21 is a schematic representation of the pFASTBAC vector containing gamma 23mer sequences and luciferase coding sequence. iPLA$_2\gamma$ sequences were inserted by ligation of 15-23mer annealed phosphorylated oligonucleotide pairs 5' of full-length luciferase coding sequence cloned into pFASTBAC via NotI/XbaI restrictions and then luciferase activity of recombinant protein produced in the Sf9 system was subsequently measured using the Luciferase Assay System of Promega.

Please delete paragraph [00060] on page 13, and replace it with the following paragraph:

[00060] Figure 23, iPLA$_2\gamma$ Repressor Region, shows phosphorylated oligo pairs for sequences between nucleotide 364 and nucleotide 455 of iPLA$_2\gamma$ for use in translational repression of ~~iPLA$_2\gamma$~~ in the luciferase expression system.

Please delete paragraph [00065] on page 13, and replace it with the following paragraph:

[00065] Figure 26, Myocardial TAG Content of Fasted WT vs iPLA$_2\gamma$ Transgenic Mice shows electrospray ionization mass spectroscopy of phospholipids in wild-type and transgenic myocardium. FIG 26(a) shows a comparison of phosphatidylcholine, ethanolamine glycerophospholipid, plasmalogen, and triacylglyceride levels in fed (open bars) and 16h fasted (closed bars) WT mice. $P< 0.01$ ($n = 3$). FIG 26(b) shows a comparison of phosphatidylcholine, ethanolamine glycerophospholipid, plasmalogen, and triacylglyceride levels in fed (open bars) and 16h fasted (closed bars) transgenic mice. $P< 0.01$. In (a) and (b), other molecular species representing <2% of the total pools were also identified without demonstrable differences between control and transgenic mice. (PC = Phosphatidylcholine, EG = Ethanolamine Glycerophospholipids, PM = Plasmalogen and TG = Triacylglyceride).

Please delete paragraph [00071] on page 15, and replace it with the following paragraph:

[00071] Figure 31, iPLA$_2\gamma$ Gamma Functional Domains, shows a diagrammatic representation of the functional domains of iPLA$_2\gamma$. The ~~dark~~ large rectangle represents the full-length iPLA$_2\gamma$ protein (SEQ ID NO: 1). The locations of alternative initiator methionine residues within the region "alternative start sites" and encoding 88kDa, 77kDa, 74kDa, and 63kDa polypeptides are indicated as 88, 77, 74, and 63 respectively. The N-terminus of the protein is also identified as the membrane binding region due to the hydrophobicity of this region of the polypeptide. Within the "alternative start site" region is the putative "inhibitory region" C-terminal of the 74kDa start site. The dark bar indicates the mitochondrial import signal and cleavage site SEQ ID NO: 95 LRK/VS. The ATP binding motif SEQ ID NO: 96 GGGTRG, lipase consensus site SEQ ID NO: 97 GVSTG, and peroxisomal localization signal site (SKL) within the "patatin homologous region" are also identified. ~~Amino acid number is indicated by the scale at the top. Sequences are shown in SEQ ID NOS 95-103, left to right, respectively, starting from the top.~~ In an aspect an amino acid number is scaled across the top. Location Label A denotes zinc finger, m0073 Transfac delta E element (transcription regulation) TCTCACCTAAG, SEQ ID NO: 98. Location Label B denotes Kringle NHGLIGILKLSTSA, SEQ ID NO: 99. Location Label C denotes SAP putative DNA binding motif KVNICM...NQNEMI, SEQ ID NO: 100, 101. Location Label D denotes Membrane retention signal ISRL, SEQ ID NO: 102. Location Label E denotes Amidation

IGKR, SEQ ID NO: 103. Location Label F denotes putative M-protein repeats (cell wall protein and virulence factor in Strep).

Please delete paragraph [00075] on page 17, and replace it with the following paragraph:

[00075] Figure 33, Promoter Analysis of iPLA$_2\gamma$ Pre exon2, shows the analysis of promoter activity of the iPLA$_2\gamma$ nucleotide sequence upstream from exon 2. Conclusion: sequence upstream of exon 2 has promoter activity. Enhancer activity resides in the region 200-400nt upstream of exon 2 (fragment IV). This region contains a CACG VNTR-like sequence as well as sequences that match consensus sites for Sp1 (8), GAGA1 (9), p300 (4), and Gcrl (10). GC regions upstream (1) and downstream (7) of this positive promoter region commonly are negative regulatory elements. Truncated fragments (II and VI) each lacking a GC region have enhanced promoter activity while fragments (III and IV) containing the GC regions but lacking region IV have minimal promoter activity. Presumably both GC regions are required for maximal inhibition. Region IV may have less than optimal promoter activity if positive promoter elements are immediately upstream or downstream of region IV.